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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/380,276A

DATE: 02/16/2001

TIME: 10:24:01

Input Set : N:\i380276.raw

Output Set: N:\CRF3\02162001\I380276A.raw

C--> 1 <110> APPLICANT: Ono Pharmaceutical Co., Ltd.
 2 <120> TITLE OF INVENTION: Novel Polypeptides, DNAs encoding the polypeptides, and utility of the
 3 Polypeptides
 4 <130> FILE REFERENCE: Q55589
 5 <140> CURRENT APPLICATION NUMBER: US/09/380,276A
 6 <141> CURRENT FILING DATE: 1997-02-27
 7 <150> PRIOR APPLICATION NUMBER: JP 9-43143
 8 <151> PRIOR FILING DATE: 1997-02-27
 9 <150> PRIOR APPLICATION NUMBER: PCT/JP98/00799
 10 <151> PRIOR FILING DATE: 1997-02-27
 11 <160> NUMBER OF SEQ ID NOS: 10
 12 <170> SOFTWARE: PatentIn version 3.0
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 15 <211> LENGTH: 1269
 16 <212> TYPE: DNA
 17 <213> ORGANISM: Homo sapiens
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 20 ggctatttgt catgtaaagt gacttgtgaa. acaggagact gtagacagca agaattcagg 120
 21 gatcgtcttg gaaactgtgt tccctgcaac cagtgtgggc caggcatgga gttgtctaag 180
 22 gaatgtggct tcggctatgg ggaggatgca cagtgtgtga cgtgccggct gcacagggttc 240
 23 aaggaggact ggggcttcca gaaatgcaag cctgtcttgg actgcgcagt ggtgaaccgc 300
 24 ttccagaagg caaattgttc agccaccagt gatgccatct gcggggactg cttgccagga 360
 25 ttttatagga agacgaaact tgtcggcttt caagacatgg agtgtgtgcc ttgtggagac 420
 26 cctcctcctc cttacgaacc gcactgtgcc agcaagggtca acctcgtgaa gatcgcgtcc 480
 27 acggcctcca gccacggga cacggcgctg gctgccgtta tctgcagcgc tctggccacc 540
 28 gtcctgctgg cctgtctcat cctctgtgtc atctattgta agagacagtt tatggagaag 600
 29 aaaccagct ggtctctgcg gtcacaggac attcagtaca acggctctga gctgtcgtgt 660
 30 cttgacagac ctacagctcca cgaatatgcc cacagagcct gctgccagtg ccgccgtgac 720
 31 tcagtgcaga ctgcggggcc ggtgcgcttg ctcccatcca tgtgctgtga ggaggcctgc 780
 32 agccccaacc cggcgactct tggttgtggg gtgcattctg cagccagtct tcaggcaaga 840
 33 aacgcaggcc cagccgggga gatggtgccg actttcttcg gatccctcac gcagtccatc 900
 34 tgtggcgagt ttccagatgc ctggcctctg atgcagaatc ccatgggtgg tgacaacatc 960
 35 tctttttgtg actcttatcc tgaactcact ggagaagaca ttattctct caatccagaa 1020
 36 cttgaaagct caacgtcttt ggattcaaat agcagtcaag atttggttgg tggggctgtt 1080
 37 ccagtccagt ctattcttga aaactttaca gcagctactg atttatctag atataacaac 1140
 38 aactggtag aatcagcatc aactcaggat gcactaacta tgagaagcca gctagatcag 1200
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 49 aagtgacttg tgaaacagga gactgtagac agcaagaatt cagggatcgg tctggaaact 180

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see p 5

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54      aacttgctcg ctttcaagac atggagtgtg tgccttgtag agaccctcct cctccttaag 480
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68      tccaccacgc cactcagacg tccctccagg aagcttaaa aacctgcttc tttctgcagt 1320
69      agaagcgtgt gctggaaccc aaagagtact cctttgttag gcttatggac tgagcagctc 1380
70      ggaccttgca tggcttcttg ggcaaaaata aatctgaacc aaactgacgg catttgaaag 1440
71      ctttcagcca gttgcttctg agccagacca gctgtaagct gaaacctcaa tgaataacaa 1500
72      gaaaagactc caggccgact catgatactc tgcattcttc ctacatgaga agcttctctg 1560
73      ccacaaaagt gacttcaaag acggatgggt tgagctggca gcctatgaga ttgtggacat 1620
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79 <212> TYPE: DNA
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82 <221> NAME/KEY: misc_feature
83 <223> OTHER INFORMATION: Origin: human bone marrow stromal cell line HAS303
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86 <221> NAME/KEY: sig_peptide
87 <222> LOCATION: (45)..(119)
88 <221> NAME/KEY: mat_peptide
89 <222> LOCATION: (120)..()
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93                                     -25
94      gtg cta cta gaa caa gag aaa acg ttt ttc act ctt tta gta tta cta 104
95      Val Leu Leu Glu Gln Glu Lys Thr Phe Phe Thr Leu Leu Val Leu Leu
96      -20 -15 -10
97      ggc tat ttg tca tgt aaa gtg act tgt gaa aca gga gac tgt aga cag 152
98      Gly Tyr Leu Ser Cys Lys Val Thr Cys Glu Thr Gly Asp Cys Arg Gln
99      -5 -1 1 5 10

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100	caa gaa ttc agg gat cgg tct gga aac tgt gtt ccc tgc aac cag tgt	200
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103	ggg cca ggc atg gag ttg tct aag gaa tgt ggc ttc ggc tat ggg gag	248
104	Gly Pro Gly Met Glu Leu Ser Lys Glu Cys Gly Phe Gly Tyr Gly Glu	
105	30 35 40	
106	gat gca cag tgt gtg acg tgc cgg ctg cac agg ttc aag gag gac tgg	296
107	Asp Ala Gln Cys Val Thr Cys Arg Leu His Arg Phe Lys Glu Asp Trp	
108	45 50 55	
109	ggc ttc cag aaa tgc aag ccc tgt ctg gac tgc gca gtg gtg aac cgc	344
110	Gly Phe Gln Lys Cys Lys Pro Cys Leu Asp Cys Ala Val Val Asn Arg	
111	60 65 70 75	
112	ttt cag aag gca aat tgt tca gcc acc agt gat gcc atc tgc ggg gac	392
113	Phe Gln Lys Ala Asn Cys Ser Ala Thr Ser Asp Ala Ile Cys Gly Asp	
114	80 85 90	
115	tgc ttg cca gga ttt tat agg aag acg aaa ctt gtc ggc ttt caa gac	440
116	Cys Leu Pro Gly Phe Tyr Arg Lys Thr Lys Leu Val Gly Phe Gln Asp	
117	95 100 105	
118	atg gag tgt gtg cct tgt gga gac cct cct cct cct tac gaa ccg cac	488
119	Met Glu Cys Val Pro Cys Gly Asp Pro Pro Pro Pro Tyr Glu Pro His	
120	110 115 120	
121	tgt gcc agc aag gtc aac ctc gtg aag atc gcg tcc acg gcc tcc agc	536
122	Cys Ala Ser Lys Val Asn Leu Val Lys Ile Ala Ser Thr Ala Ser Ser	
123	125 130 135	
124	cca cgg gac acg gcg ctg gct gcc gtt atc tgc agc gct ctg gcc acc	584
125	Pro Arg Asp Thr Ala Leu Ala Ala Val Ile Cys Ser Ala Leu Ala Thr	
126	140 145 150 155	
127	gtc ctg ctg gcc ctg ctc atc ctc tgt gtc atc tat tgt aag aga cag	632
128	Val Leu Leu Ala Leu Ile Leu Cys Val Ile Tyr Cys Lys Arg Gln	
129	160 165 170	
130	ttt atg gag aag aaa ccc agc tgg tct ctg cgg tca cag gac att cag	680
131	Phe Met Glu Lys Lys Pro Ser Trp Ser Leu Arg Ser Gln Asp Ile Gln	
132	175 180 185	
133	tac aac ggc tct gag ctg tgc tgt ctt gac aga cct cag ctc cac gaa	728
134	Tyr Asn Gly Ser Glu Leu Ser Cys Leu Asp Arg Pro Gln Leu His Glu	
135	190 195 200	
136	tat gcc cac aga gcc tgc tgc cag tgc cgc cgt gac tca gtg cag acc	776
137	Tyr Ala His Arg Ala Cys Cys Gln Cys Arg Arg Asp Ser Val Gln Thr	
138	205 210 215	
139	tgc ggg ccg gtg cgc ttg ctc cca tcc atg tgc tgt gag gag gcc tgc	824
140	Cys Gly Pro Val Arg Leu Leu Pro Ser Met Cys Cys Glu Glu Ala Cys	
141	220 225 230 235	
142	agc ccc aac ccg gcg act ctt ggt tgt ggg gtg cat tct gca gcc agt	872
143	Ser Pro Asn Pro Ala Thr Leu Gly Cys Gly Val His Ser Ala Ala Ser	
144	240 245 250	
145	ctt cag gca aga aac gca ggc cca gcc ggg gag atg gtg ccg act ttc	920
146	Leu Gln Ala Arg Asn Ala Gly Pro Ala Gly Glu Met Val Pro Thr Phe	
147	255 260 265	
148	ttc gga tcc ctc acg cag tcc atc tgt ggc gag ttt tca gat gcc tgg	968

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152   Pro Leu Met Gln Asn Pro Met Gly Gly Asp Asn Ile Ser Phe Cys Asp
153           285                290                295
154   tct tat cct gaa ctc act gga gaa gac att cat tct ctc aat cca gaa      1064
155   Ser Tyr Pro Glu Leu Thr Gly Glu Asp Ile His Ser Leu Asn Pro Glu
156   300                305                310                315
157   ctt gaa agc tca acg tct ttg gat tca aat agc agt caa gat ttg gtt      1112
158   Leu Glu Ser Ser Thr Ser Leu Asp Ser Asn Ser Ser Gln Asp Leu Val
159           320                325                330
160   ggt ggg gct gtt cca gtc cag tct cat tct gaa aac ttt aca gca gct      1160
161   Gly Gly Ala Val Pro Val Gln Ser His Ser Glu Asn Phe Thr Ala Ala
162           335                340                345
163   act gat tta tct aga tat aac aac aca ctg gta gaa tca gca tca act      1208
164   Thr Asp Leu Ser Arg Tyr Asn Asn Thr Leu Val Glu Ser Ala Ser Thr
165           350                355                360
166   cag gat gca cta act atg aga agc cag cta gat cag gag agt ggc gct      1256
167   Gln Asp Ala Leu Thr Met Arg Ser Gln Leu Asp Gln Glu Ser Gly Ala
168           365                370                375
169   atc atc cac cca gcc act cag acg tcc ctc cag gaa gct taaagaacct      1305
170   Ile Ile His Pro Ala Thr Gln Thr Ser Leu Gln Glu Ala
171   380                385                390
172   gcttcttttct gcagtagaag cgtgtgctgg aacccaaaga gtactccttt gttaggctta      1365
173   tggactgagc agtctggacc ttgcatggct tctggggcaa aaataaatct gaaccaaact      1425
174   gacggcattt gaagcctttc agccagttgc ttctgagcca gaccagctgt aagctgaaac      1485
175   ctcaatgaat aacaagaaaa gactccaggc cgactcatga tactctgcat ctttcttaca      1545
176   tgagaagctt ctctgccaca aaagtgactt caaagacgga tgggttgagc tggcagccta      1605
177   tgagattgtg gacatataac aagaaacaga aatgccctca tgcttatttt catggtgatt      1665
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183 <213> ORGANISM: Homo sapiens
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185 <221> NAME/KEY: misc_feature
186 <223> OTHER INFORMATION: Origin: human bone marrow stromal cell line HAS303
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191           -5                -1 1                5
192   Asp Cys Arg Gln Gln Glu Phe Arg Asp Arg Ser Gly Asn Cys Val Pro
193           10                15                20
194   Cys Asn Gln Cys Gly Pro Gly Met Glu Leu Ser Lys Glu Cys Gly Phe
195           25                30                35
196   Gly Tyr Gly Glu Asp Ala Gln Cys Val Thr Cys Arg Leu His Arg Phe
197           40                45                50                55
198   Lys Glu Asp Trp Gly Phe Gln Lys Cys Lys Pro Cys Leu Asp Cys Ala

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203          90          95          100
204  Gly Phe Gln Asp Met Glu Cys Val Pro Cys Gly Asp Pro Pro Pro Pro
205          105          110          115
206  Tyr Glu Pro His Cys Ala Ser Lys Val Asn Leu Val Lys Ile Ala Ser
207          120          125          130          135
208  Thr Ala Ser Ser Pro Arg Asp Thr Ala Leu Ala Ala Val Ile Cys Ser
209          140          145          150
210  Ala Leu Ala Thr Val Leu Leu Ala Leu Leu Ile Leu Cys Val Ile Tyr
211          155          160          165
212  Cys Lys Arg Gln Phe Met Glu Lys Lys Pro Ser Trp Ser Leu Arg Ser
213          170          175          180
214  Gln Asp Ile Gln Tyr Asn Gly Ser Glu Leu Ser Cys Leu Asp Arg Pro
215          185          190          195
216  Gln Leu His Glu Tyr Ala His Arg Ala Cys Cys Gln Cys Arg Arg Asp
217          200          205          210          215
218  Ser Val Gln Thr Cys Gly Pro Val Arg Leu Leu Pro Ser Met Cys Cys
219          220          225          230
220  Glu Glu Ala Cys Ser Pro Asn Pro Ala Thr Leu Gly Cys Gly Val His
221          235          240          245
222  Ser Ala Ala Ser Leu Gln Ala Arg Asn Ala Gly Pro Ala Gly Glu Met
223          250          255          260
224  Val Pro Thr Phe Phe Gly Ser Leu Thr Gln Ser Ile Cys Gly Glu Phe
225          265          270          275
226  Ser Asp Ala Trp Pro Leu Met Gln Asn Pro Met Gly Gly Asp Asn Ile
227          280          285          290          295
228  Ser Phe Cys Asp Ser Tyr Pro Glu Leu Thr Gly Glu Asp Ile His Ser
229          300          305          310
230  Leu Asn Pro Glu Leu Glu Ser Ser Thr Ser Leu Asp Ser Asn Ser Ser
231          315          320          325
232  Gln Asp Leu Val Gly Gly Ala Val Pro Val Gln Ser His Ser Glu Asn
233          330          335          340
234  Phe Thr Ala Ala Thr Asp Leu Ser Arg Tyr Asn Asn Thr Leu Val Glu
235          345          350          355
236  Ser Ala Ser Thr Gln Asp Ala Leu Thr Met Arg Ser Gln Leu Asp Gln
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243 <211> LENGTH: 1269
244 <212> TYPE: DNA
245 <213> ORGANISM: Homo sapiens
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY DATE: 02/16/2001
PATENT APPLICATION: US/09/380,276A TIME: 10:24:02

Input Set : N:\i380276.raw
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L:6 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:474 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:9
L:474 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:9